

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: CHAPMAN, BARBARA  
BURKE, RAE LYN  
RASMUSSEN, MIRELLA EZBAN  
MIKKELSON, JAN MOLLER

(ii) TITLE OF INVENTION: PROTEIN COMPLEXES HAVING FACTOR VIII:C  
ACTIVITY AND PRODUCTION THEREOF

(iii) NUMBER OF SEQUENCES: 35

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: REED & ROBINS  
(B) STREET: 285 HAMILTON AVENUE, SUITE 200  
(C) CITY: PALO ALTO  
(D) STATE: CALIFORNIA  
(E) COUNTRY: UNITED STATES OF AMERICA  
(F) ZIP: 94301

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: PC-DOS/MS-DOS  
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/441,943  
(B) FILING DATE: 16-MAY-1995  
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 051,916  
(B) FILING DATE: 19-MAY-1987

(viii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 822,989  
(B) FILING DATE: 27-JAN-1986

(ix) ATTORNEY/AGENT INFORMATION:

(A) NAME: BAROVSKY, KENNETH  
(B) REGISTRATION NUMBER: 36,442  
(C) REFERENCE/DOCKET NUMBER: 2300-0048.10

(x) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (415) 327-3400  
(B) TELEFAX: (415) 327-3231

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 30 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: misc\_difference
- (B) LOCATION: replace(1..4, "")
- (D) OTHER INFORMATION: /note= "Overhang: not paired with complimentary strand."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

AGCTAGATCT CCCGGGTCTA GATAAGTAAT

30

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: misc\_difference
- (B) LOCATION: replace(1..4, "")
- (D) OTHER INFORMATION: /note= "Overhang: not paired with complimentary strand."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

GATCATTACT TATCTAGACC CGGGAGATCT

30

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

AGATCTCGAA TTCCCCGGGG GTACCT

26

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: misc\_difference
- (B) LOCATION: replace(1..4, "")
- (D) OTHER INFORMATION: /note= "Overhang: not paired with complimentary strand."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

CTAGAGGTAC CCCCGGGGAA TTCGAGATCT

30

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: misc\_difference
- (B) LOCATION: replace(1..4, "")
- (D) OTHER INFORMATION: /note= "Overhang: not paired with complimentary strand."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GATCTCGAAT TCCCCGGGTC TAGAGGATCC GTCGAC

36

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: misc\_difference
- (B) LOCATION: replace(1..4, "")
- (D) OTHER INFORMATION: /note= "Overhang: not paired with complimentary strand."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

CTAGGTGCAC GGATCCTCTA GACCCGGGGA ATTCTGA

36

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 49 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: misc\_difference
- (B) LOCATION: replace(1..4, "")
- (D) OTHER INFORMATION: /note= "Overhang: not paired with complimentary strand."

(ix) FEATURE:  
(A) NAME/KEY: CDS  
(B) LOCATION: 36..47

(ix) FEATURE:  
(A) NAME/KEY: misc\_difference  
(B) LOCATION: replace(46..49, "")  
(D) OTHER INFORMATION: /note= "Overhang: not paired with  
complimentary strand."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GATCCTCTCC AGTTAACAT TTGTAGCAAT AAGTC ATG CAA ATA GAG CT  
Met Gln Ile Glu  
1

49

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 4 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met Gln Ile Glu  
1

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 41 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

CTATTTGCAT GACTTATTGC TACAAATGTT CAACTGGAGA G

41

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 9 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

GTCATGCAA

9

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 7 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

ACCATGG

7

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 135 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: CDS  
(B) LOCATION: 1..135

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

ATG GAT GCA ATG AAG AGA GGG CTC TGC TGC TGT GTG CTG CTG TGT GGA  
Met Asp Ala Met Lys Arg Gly Leu Cys Cys Val Leu Leu Cys Gly  
1 5 10 15

48

GCA GTC TTC GTT TCG CCC AGC CAG GAA ATC CAT GCC CGA TTC AGA AGA  
Ala Val Phe Val Ser Pro Ser Gln Glu Ile His Ala Arg Phe Arg Arg  
20 25 30

96

GGA GCC AGA TCT ATA ACT CGT ACT CTT CAG CAG TCT GAT  
Gly Ala Arg Ser Ile Thr Arg Thr Leu Gln Gln Ser Asp  
35 40 45

135

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 45 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Met Asp Ala Met Lys Arg Gly Leu Cys Cys Val Leu Leu Cys Gly  
1 5 10 15

Ala Val Phe Val Ser Pro Ser Gln Glu Ile His Ala Arg Phe Arg Arg  
20 25 30

Gly Ala Arg Ser Ile Thr Arg Thr Leu Gln Gln Ser Asp  
35 40 45

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 135 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..135

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

ATG GAT GCA ATG AAG AGA GGG CTC TGC TGC TGT GTG CTG CTG TGT GGA	48
Met Asp Ala Met Lys Arg Gly Leu Cys Cys Cys Val Leu Leu Cys Gly	
1 5 10 15	
GCA GTC TTC GTT TCG CCC AGC CAG GAA ATC CAT GCC CGA TTC AGA AGA	96
Ala Val Phe Val Ser Pro Ser Gln Glu Ile His Ala Arg Phe Arg Arg	
20 25 30	
GGA GCC AGA GAA ATA ACT CGT ACT CTT CAG CAG TCT GAT	135
Gly Ala Arg Glu Ile Thr Arg Thr Leu Gln Gln Ser Asp	
35 40 45	

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Met Asp Ala Met Lys Arg Gly Leu Cys Cys Cys Val Leu Leu Cys Gly	
1 5 10 15	
Ala Val Phe Val Ser Pro Ser Gln Glu Ile His Ala Arg Phe Arg Arg	
20 25 30	
Gly Ala Arg Glu Ile Thr Arg Thr Leu Gln Gln Ser Asp	
35 40 45	

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 126 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..126

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

ATG GAT GCA ATG AAG AGA GGG CTC TGC TGC TGT GTG CTG CTG TGT GGA	48
Met Asp Ala Met Lys Arg Gly Leu Cys Cys Cys Val Leu Leu Cys Gly	
1 5 10 15	
GCA GTC TTC GTT TCG CCC AGC GAG ATA ACT CGT ACT CTT CAG CAG TCT	96
Ala Val Phe Val Ser Pro Ser Glu Ile Thr Arg Thr Leu Gln Gln Ser	
20 25 30	
GAT CAA GAG GAA ATT GAC TAT GAT GAT ACC	126
Asp Gln Glu Glu Ile Asp Tyr Asp Asp Thr	
35 40	

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 42 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Met Asp Ala Met Lys Arg Gly Leu Cys Cys Cys Val Leu Leu Cys Gly	
1 5 10 15	
Ala Val Phe Val Ser Pro Ser Glu Ile Thr Arg Thr Leu Gln Gln Ser	
20 25 30	
Asp Gln Glu Glu Ile Asp Tyr Asp Asp Thr	
35 40	

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 126 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..126

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

ATG GAT GCA ATG AAG AGA GGG CTC TGC TGC TGT GTG CTG CTG TGT GGA	48
Met Asp Ala Met Lys Arg Gly Leu Cys Cys Cys Val Leu Leu Cys Gly	
1 5 10 15	
GCA GTC TTC GTT TCG CCC AGC CAG GAA ATC CAT GCC CGA TTC AGA AGA	96
Ala Val Phe Val Ser Pro Ser Gln Glu Ile His Ala Arg Phe Arg Arg	
20 25 30	
GAG ATA ACT CGT ACT CTT CAG CAG TCT GAT	126
Glu Ile Thr Arg Thr Leu Gln Gln Ser Asp	
35 40	

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 42 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

Met Asp Ala Met Lys Arg Gly Leu Cys Cys Cys Val Leu Leu Cys Gly  
1 5 10 15

Ala Val Phe Val Ser Pro Ser Gln Glu Ile His Ala Arg Phe Arg Arg  
20 25 30

Glu Ile Thr Arg Thr Leu Gln Gln Ser Asp  
35 40

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 126 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: CDS  
(B) LOCATION: 1..126

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

ATG GAT GCA ATG AAG AGA GGG CTC TGC TGC TGT GTG CTG CTG TGT GGA 48  
Met Asp Ala Met Lys Arg Gly Leu Cys Cys Cys Val Leu Leu Cys Gly  
1 5 10 15

GCA GTC TTC GTT TCG CCC AGC CAG GAA ATC CAT GCC GAG ATA ACT CGT 96  
Ala Val Phe Val Ser Pro Ser Gln Glu Ile His Ala Glu Ile Thr Arg  
20 25 30

ACT CTT CAG CAG TCT GAT CAA GAG GAA ATT 126  
Thr Leu Gln Gln Ser Asp Gln Glu Glu Ile  
35 40

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 42 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

Met Asp Ala Met Lys Arg Gly Leu Cys Cys Cys Val Leu Leu Cys Gly  
1 5 10 15

Ala Val Phe Val Ser Pro Ser Gln Glu Ile His Ala Glu Ile Thr Arg  
20 25 30

Thr Leu Gln Gln Ser Asp Gln Glu Glu Ile  
35 40

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

Xaa Ile Xaa Arg Thr Xaa Leu Gln Xaa Asp Gln  
1 5 10

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

Xaa Xaa Arg Glu Ile Thr Arg Thr Thr Leu  
1 5 10

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

Ser Glu Ile Thr Arg Thr  
1 5

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 4 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

Xaa Gln Glu Ile  
1

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 135 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: CDS  
(B) LOCATION: 1..135

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

ATG CCC TCG AGC GTC TCG TGG GGC ATC CTC CTG CTG GCA GGC CTG TGC	48
Met Pro Ser Ser Val Ser Trp Gly Ile Leu Leu Leu Ala Gly Leu Cys	
1 5 10 15	
TGC CTG GTC CCT GTC TCC CTG GCT GAG ATC ACT CGT ACT ACT CTT CAG	96
Cys Leu Val Pro Val Ser Leu Ala Glu Ile Thr Arg Thr Thr Leu Gln	
20 25 30	
TCT GAT CAA GAG GAA ATT GAC TAT GAT GAT ACC ATA TCA	135
Ser Asp Gln Glu Ile Asp Tyr Asp Asp Thr Ile Ser	
35 40 45	

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 45 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

Met Pro Ser Ser Val Ser Trp Gly Ile Leu Leu Leu Ala Gly Leu Cys	
1 5 10 15	
Cys Leu Val Pro Val Ser Leu Ala Glu Ile Thr Arg Thr Thr Leu Gln	
20 25 30	
Ser Asp Gln Glu Ile Asp Tyr Asp Asp Thr Ile Ser	
35 40 45	

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

Glu Ile Thr Arg Thr Xaa Leu Gln Ser Asp Gln  
1 5 10

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 109 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: misc\_difference
- (B) LOCATION: replace(1..4, "")
- (D) OTHER INFORMATION: /note= "Overhang: not paired with complimentary strand."

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..102

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

AGC TTC TCC CAG AAT TCT AGA CAC CCT AGC ACT AGG CAA AAG CAA TTT Ser Phe Ser Gln Asn Ser Arg His Pro Ser Thr Arg Gln Lys Gln Phe	48
1 5 10 15	
AAT GCC ACC CCT CCT ACA CCA CCA ACC CCA CCA GTA CTG AAA CGC CAT Asn Ala Thr Pro Pro Thr Pro Pro Val Leu Lys Arg His	96
20 25 30	
CAA CGG TGATAAG Gln Arg	109

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

Ser Phe Ser Gln Asn Ser Arg His Pro Ser Thr Arg Gln Lys Gln Phe  
1 5 10 15

Asn Ala Thr Pro Pro Thr Pro Pro Thr Pro Pro Val Leu Lys Arg His  
20 25 30

Gln Arg

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 109 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: misc\_difference
- (B) LOCATION: replace(1..4, "")
- (D) OTHER INFORMATION: /note= "Overhang: not paired with complimentary strand."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

TCGACTTATC ACCGTTGATG GCGTTTCAGT ACTGGTGGGG TTGGTGGTGT AGGAGGGGTG 60

GCATTAATT GCTTTTGCT AGTGCTAGGG TGTCTAGAAT TCTGGGAGA 109

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

Ser Phe Ser Gln Asn Ser Arg His Pro Ser Thr Arg Gln Lys Gln Phe  
1 5 10 15

Asn Ala Thr

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

Pro Pro Thr Pro Pro Thr  
1 5

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 9 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

Pro Pro Val Leu Lys Arg His Gln Arg  
1 5

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 23 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

Met Pro Ser Ser Val Ser Trp Gly Ile Leu Leu Ala Gly Leu Cys Cys  
1 5 10 15

Leu Val Pro Val Ser Leu Ala  
20